

GenCore version 5.1.4.p5.4578  
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## OM protein - protein search, using sw model

Run on: March 17, 2003, 08:47:27 ; Search time 35 Seconds  
(without alignments)  
4580.133 Million cell updates/sec

Title: US-10-010-227-3

Perfect score: 4055

Sequence: 1 MCGAESTPQTLVDKVLQAHV.....KAVPVPPTNRGEEKPELW 778

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database :

SPTREMBL\_21:\*  
1: sp archaea:\*  
2: sp bacteria:\*  
3: sp fungi:\*  
4: sp human:\*  
5: sp invertebrate:\*  
6: sp mammal:\*  
7: sp mhc:\*  
8: sp organelle:\*  
9: sp phage:\*  
10: sp plant:\*  
11: sp rodent:\*  
12: sp virus:\*  
13: sp vertebrate:\*  
14: sp unclassified:\*  
15: sp virus:\*  
16: sp bacteriap:\*  
17: sp archaeap:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	length	ID	Description
1	2432.5	60.0	711	3	Q9P3Y5	Q9P3Y5 yarrowia li
2	1636	40.3	469	16	Q92L76	Q92L76 rhizobium m
3	1611	39.7	469	16	Q8YJC9	Q8YJC9 bruceella me
4	1586	39.1	475	16	Q8UBV9	Q8UBV9 agrobacteri
5	1567.5	38.7	468	16	Q9SEB1	Q9SEB1 rhizobium l
6	1563	38.5	449	2	Q9EV53	Q9EV53 rhizobium m
7	1562	38.5	479	16	Q9ABN0	Q9ABN0 caulobacter
8	1548.5	38.2	469	16	Q9JZ15	Q9JZ15 neisseria m
9	1545.5	38.1	469	16	Q9JUB2	Q9JUB2 neisseria m
10	1507.5	37.2	474	16	Q9HZA3	Q9HZA3 pseudomonas
11	1498.5	37.0	474	16	Q9PAX0	Q9PAX0 xylella fas
12	1493	36.8	469	16	Q8XXX3	Q8XXX3 ralestonia s
13	1469.5	36.2	466	16	Q8XAO0	Q8XAO0 escherichia
14	1452	35.8	476	16	Q8ZIH0	Q8ZIH0 yersinia pe
15	1425.5	35.2	467	16	Q9KPB1	Q9KPB1 vibrio chol
16	1396	34.4	472	16	Q9K8P0	Q9K8P0 bacillus ha

17	1385.5	34.2	476	16	Q86534	Q86534 streptomyce
18	1354.5	33.4	466	2	Q85072	Q85072 buchnera ap
19	1354	33.4	469	2	Q85065	Q85065 buchnera ap
20	1315.5	32.4	448	2	Q9EVF9	Q9EVF9 buchnera ap
21	1311.5	32.3	470	16	Q9P1M1	Q9P1M1 campylobact
22	1290.5	31.8	466	2	Q31293	Q31293 buchnera ap
23	1283.5	31.7	462	16	Q92A26	Q92A26 listeria in
24	1282	31.6	442	2	Q9ESJ3	Q9ESJ3 staphylococ
25	1280.5	31.6	442	2	Q9EVH1	Q9EVH1 buchnera ap
26	1279.5	31.6	462	16	Q8YSR7	Q8YSR7 listeria mo
27	1275.5	31.5	443	2	Q9EVI0	Q9EVI0 buchnera ap
28	1271.5	31.4	444	2	Q9EVG8	Q9EVG8 buchnera ap
29	1259.5	31.1	443	2	Q9EVG5	Q9EVG5 buchnera ap
30	1253.5	30.9	443	2	Q9EVI6	Q9EVI6 buchnera ap
31	1252.5	30.9	442	2	Q9EVI3	Q9EVI3 buchnera ap
32	1244.5	30.7	436	2	Q9AJ49	Q9AJ49 buchnera ap
33	1240.5	30.6	436	2	Q9AJ48	Q9AJ48 buchnera ap
34	1238.5	30.5	436	2	Q99073	Q99073 buchnera ap
35	1238.5	30.5	436	2	Q9AJ47	Q9AJ47 buchnera ap
36	1236.5	30.5	443	2	Q9EVA4	Q9EVA4 buchnera ap
37	1230.5	30.3	436	2	Q9AJS2	Q9AJS2 buchnera ap
38	1227.5	30.3	442	2	Q9EVS7	Q9EVS7 buchnera ap
39	1225.5	30.2	444	2	Q9EVB0	Q9EVB0 buchnera ap
40	1222.5	30.1	433	2	Q99009	Q99009 buchnera ap
41	1217.5	30.0	473	16	Q8ZRU0	Q8ZRU0 salmonella
42	1211.5	29.9	442	2	Q9EVS2	Q9EVS2 buchnera ap
43	1209.5	29.8	472	2	Q9ZND5	Q9ZND5 thermus the
44	1194.5	29.5	456	2	Q9A1M3	Q9A1M3 streptococc
45	1172.5	28.9	467	16	Q8YX02	Q8YX02 anabaena sp
46	1170.5	28.9	418	2	Q9AJS0	Q9AJS0 buchnera ap
47	1065.5	26.3	369	2	Q9AQC6	Q9AQC6 buchnera ap
48	699.5	17.3	418	17	Q8TVF2	Q8TVF2 methanopyru
49	660	16.3	424	17	Q8TLF1	Q8TLF1 methanosarc
50	656.5	16.2	424	17	Q8UZA1	Q8UZA1 pyrococcus
51	641	15.8	431	16	Q9RTI6	Q9RTI6 deinococcus
52	640.5	15.8	653	16	Q67656	Q67656 aquifex aeo
53	637.5	15.7	423	17	Q9UD07	Q9UD07 pyrococcus
54	627.5	15.5	174	2	Q8VMA6	Q8VMA6 rhizobium e
55	612.5	15.1	641	16	Q8RCF8	Q8RCF8 thermoaer
56	599	14.8	642	16	Q97KE8	Q97KE8 clostridium
57	597.5	14.7	211	16	Q8YCW7	Q8YCW7 bruceella me
58	595.5	14.7	417	16	Q9WZ24	Q9WZ24 thermotoga
59	586.5	14.5	201	16	Q98BS1	Q98BS1 rhizobium l
60	576.5	14.2	422	16	Q97BE0	Q97BE0 clostridium
61	570.5	14.1	509	10	Q94AR8	Q94AR8 arabidopsis
62	562	13.9	420	17	Q8TQZ3	Q8TQZ3 methanosarc
63	562	13.9	661	17	Q9HMF1	Q9HMF1 halobacteri
64	560.5	13.8	216	16	Q8UBR0	Q8UBR0 agrobacteri
65	558.5	13.8	509	10	Q9TOL4	Q9TOL4 arabidopsis
66	555.5	13.7	201	16	Q92LA1	Q92LA1 rhizobium m
67	552	13.6	721	3	Q9UT74	Q9UT74 schizosacch
68	544	13.4	213	16	Q9JUB1	Q9JUB1 neisseria m
69	542	13.4	212	16	Q9HZA4	Q9HZA4 pseudomonas
70	542	13.4	213	16	Q9JZ16	Q9JZ16 neisseria m
71	541.5	13.4	418	16	Q9WTC7	Q9WTC7 thermotoga
72	536.5	13.2	777	3	Q96VU1	Q96VU1 aspergillus
73	535	13.1	216	16	Q8XXX4	Q8XXX4 ralestonia s
74	533	13.2	201	2	Q8P9E8	Q8P9E8 methylobact
75	523.5	12.9	418	2	Q9ZNE0	Q9ZNE0 thermus the
76	519	12.8	215	16	Q9PAX1	Q9PAX1 xylella fas
77	513	12.7	202	16	Q9ABN1	Q9ABN1 caulobacter
78	512	12.6	434	16	Q9RTY9	Q9RTY9 deinococcus
79	511.5	12.6	418	16	Q8RDK2	Q8RDK2 thermoaer
80	506	12.5	201	16	Q8ZJ13	Q8ZJ13 salmonella
81	500.5	12.3	201	16	Q9CJN8	Q9CJN8 pasteurella
82	498	12.3	200	16	Q9XP80	Q9XP80 vibrio chol
83	492	12.1	201	16	Q8XA01	Q8XA01 escherichia
84	482.5	11.9	768	4	Q9UGZ0	Q9UGZ0 homo sapien
85	474.5	11.7	780	4	Q8TA06	Q8TA06 homo sapien
86	474	11.7	200	16	Q8ZIH0	Q8ZIH0 yersinia pe
87	473.5	11.7	780	11	Q99K10	Q99K10 mus musculu
88	472.5	11.7	780	11	Q9ER34	Q9ER34 ratus norv
89	472.5	11.7	787	5	Q9NFX1	Q9NFX1 drosophila

90 470.5 11.6 778 3 074699  
 91 467 11.5 194 16 Q9K8F1  
 92 463 11.4 905 3 Q9P7D4  
 93 457 11.3 809 3 Q9HEA5  
 94 455 11.2 788 5 Q9NG03  
 95 447 11.0 748 5 Q8ZM41  
 96 442.5 10.9 747 2 Q8R887  
 97 442 10.9 683 5 Q9VIE8  
 98 441 10.9 402 17 Q8TW29  
 99 440 10.9 415 17 Q974R0  
 100 438 10.8 196 2 Q9AIM2

## ALIGNMENTS

## RESULT 1

Q9P3Y5  
 ID Q9P3Y5 PRELIMINARY; PRT; 711 AA.  
 AC Q9P3Y5  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE 3-isopropylmalate dehydratase (EC 4.2.1.33) (Fragment).  
 GN LEU1.  
 OS Yarrowia lipolytica (Candida lipolytica).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Dipodascaceae; Yarrowia.  
 OX NCBI\_TaxID=4952;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=R22;  
 RX MEDLINE=21382182; PubMed=11489863;  
 RA Mautersberger S., Wang H., Gaillardin C., Barth G., Nicaud J.M.,  
 RT "Inertional mutagenesis in the n-alkane-assimilating yeast Yarrowia  
 RT lipolytica: generation of tagged mutations in genes involved in  
 RT hydrophobic substrate utilization."  
 RL J. Bacteriol. 183:5102-5109(2001).  
 DR EMBL; AJ278693; CAB99455.1; -  
 DR InterPro; IPR000573; Aconitase\_C.  
 DR InterPro; IPR001030; Aconitase\_N.  
 DR InterPro; IPR001899; Gram\_pos\_anchor.  
 DR InterPro; IPR004430; Leuc.  
 DR InterPro; IPR004431; Leuc.  
 DR Pfam; PF00330; aconitase; 1.  
 DR PRINTS; PR00694; Aconitase\_C; 1.  
 DR PRODOM; PD000511; Aconitase\_N; 1.  
 DR TIGRFAMs; TIGR00170; leuc; 1.  
 DR TIGRFAMs; TIGR00171; leuc; 1.  
 DR PROSITE; PS00450; ACONITASE\_1; 1.  
 DR PROSITE; PS01244; ACONITASE\_2; 1.  
 DR PROSITE; PS00343; GRAM\_POS\_ANCHORING; UNKNOWN\_1.  
 KW Lyase.  
 FT NON\_TER  
 SQ SEQUENCE 711 AA; 77476 MW; 996407A7F7B1AF2E CRC64;

Query Match  
 Best Local Similarity 60.0%; Score 2432.5; DB 3; Length 711;  
 Matches 480; Conservative 76; Mismatches 130; Indels 45; Gaps 9;

QY 9 QLYDKVLQAHVDEKLDGTVLYIDRLVHEVTSPOAFGLRNAGKVRPDCITLATD 68  
 DB 3 QLYDKVFAHDVHHED - NGTYLLFIDRLVHEVTSPOAFGLRNAGKVRPDCITLATD 61  
 QY 69 HNVPTTSRKALDIAGFIKEDDSRTQCVLENNKFGVTVFGLSDKRGVHVHVGIEQG 128  
 DB 62 HNIPTTRKDFKISGFIKEEDSRLOCTILEQNVKFGVTVFGLSDKRGVHVHVGIEQG 121  
 QY 129 FTLPGTVVCGSDHSTHGAFGALFAGIGTSVEHVLATQCLITKRSKNRIQVDGELAP 188  
 DB 122 FTLPGTVVCGSDHSTHGAFGALFAGIGTSVEHVLATQCLITKRSKNRIQVDGELAP 181

QY 189 GVSSKDVVLHAIGITAGGTGAVIEFCGSVIRLSNEARMSTCNMSIEGAGARAGVAPD 248  
 DB 182 GITSKDLILHIIIGVITAGGTGAVIEFCGEAIRDLSEARMSCMNAIEGAGARAGVAPD 241  
 QY 249 EITFEVLGRPLAPKYDSEWHEKATQYKNLQSDPCAKYDIDYFIDAKDIPVLTWTGTS 308  
 DB 242 EITFYIRGRPLAP - EGAEWEKAVTYKTLHSDSDAEFDIDVNIKGEDIIPTVTWTGTS 299  
 QY 309 EDVPIITGVVDPETFATEAKKADGRMLQYMLKAGTMEIDIPDKVFGISCTNSRIED 368  
 DB 300 QDALPITGVDPDSKESDPIKRAGIERALEYMGLEANTPLNEIAVDKVFISCTNSRIED 359  
 QY 369 LRAAAVVKGRKAPNVKSAMVVPVSGLVKTOAEBEGLDKIPFEAGFEWREAGSCMLGM 428  
 DB 360 LRAAAAVIRGKKKADSVVRAMVVPVSGLVKRAEAEGLDKVFEAGFEWREAGSCMLGM 419  
 QY 429 NPDILAPOBCASTSNRNPEGRGAGGRTHLMSPVMAAAGIVGKLADVR - - - - - KL 480  
 DB 420 NPDILNPRECASTSNRNPEGRGAGGRTHLMSPVMAAAGIVGKLADVR - - - - - 479  
 QY 481 T - - - - - DYKASPHIAAYOKSTVTKPH - VDERINQDAHEKDIADIPEDNNGPH 527  
 DB 480 VIGEDEMAEAKYDEKQPAVKMKMTATVTQADPVDEQTDVAEE - - - - - 524  
 QY 528 TNSASVGTSGAGLPKPTILKIGIAAPLEKANVDTDAIPKQFLKTIKRTGLGNALFVEMRF 587  
 DB 525 -NITSS - - - - - ATGIPKFLVSGIAAPLPKANVDTDAIPKQFLKTIKRTGLSSGLFEWRF 580  
 QY 588 NE-DG - TEKSDFLNKEPVYRKASILVCTGANFGCGSSREHAPWALNDFGIRSVIAPSPAD 645  
 DB 581 KEVDGQKERTDFMLNVPWPDWKASILVSGNFGCGSSREHAPWALNDFGIRSVIAPSPAD 640  
 QY 646 IFFNNSFKNGMLPIPIKQAOIAEIAAEARAGKEVDPNLIKKNATGETICTFEVEEF 705  
 DB 641 IFFNNSFKNGMLPIRVDADVIKSLMPVADKGSLSLTVDLPNQKVLHGDEVLDHFEVEDP 700  
 QY 706 RKHCLVNGLDD 716  
 DB 701 RKHCRVNGLDD 711  
 RESULT 2  
 Q92L76 PRELIMINARY; PRT; 469 AA.  
 ID Q92L76  
 AC Q92L76;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Probable 3-isopropylmalate dehydratase large subunit protein  
 DE (EC 4.2.1.33).  
 GN LEUC OR R03206 OR SMC03823.  
 OS Rhizobium meliloti (Sinorhizobium meliloti).  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Rhizobiaceae; Sinorhizobium.  
 OX NCBI\_TaxID=382;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=1021;  
 RX MEDLINE=21396507; PubMed=11481430;  
 RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,  
 RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,  
 RA Goidre T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masny D.,  
 RA Pohl T., Portetelle D., Puehler A., Purnelle B., Rameger U.,  
 RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.,  
 RT "Analysis of the chromosome sequence of the legume symbiont  
 RT Sinorhizobium meliloti strain 1021".  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).  
 DR EMBL; AL591793; CAC47785.1; -  
 DR InterPro; IPR001030; Aconitase\_N.  
 DR Pfam; PF00330; aconitase; 1.  
 DR PRODOM; PD000511; Aconitase\_N; 1.  
 DR TIGRFAMs; TIGR00170; leuc; 1.



RA	Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,
RA	Takeuchi C., Yamada M., Tabata S.;
RT	"Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT	Mesorhizobium loti.";
RL	DNA Res. 7:331-338 (2000).
DR	EMBL; AP003003; BAB5968.1; -.
DR	InterPro; IPR001030; Aconitase_N.
DR	InterPro; IPR004430; Leuc.
DR	Pfam; PF00330; aconitase; 1.
DR	PRINTS; PR00415; ACONITASE.
DR	ProDom; PD005511; Aconitase_N; 1.
DR	TIGRFAMs; TIGR00170; leuc; 1.
DR	PROSITE; PS00450; ACONITASE_1.
DR	PROSITE; PS01244; ACONITASE_2; UNKNOWN_1.
KW	Complete proteome.
SQ	SEQUENCE 469 AA; 50871 MW; 641532D3D4F06888 CRC64;

  

Query Match	38.7%; Score 1567.5; DB 16; Length 469;
Best Local Similarity	64.1%; Pred.No. 1.4e-97;
Matches 307; Conservative 53; Mismatches 108; Indels 11; Gaps	

  

Qy	6	STPOTLYDKVLQAHVDEKLDGTIVLLYIDRHLYHEVTSPQAPEGLRNAGRKVRPPDCTLA 65
Db	2	SAPRTLTKDFDDHWVDRODGGTCLLYIDRHLYHEVTSPQAPEGLSLGRKVRHPEKTLA 61
		:    :    :    :    :    :    :    :    :    :    :    :    :    :
Qy	66	TTDHNVPFTSRKALKIASFIKEDDSRTCQCVTLEENKKEGVTFYFGLSKRGQGHVHVG 125
		:    :    :    :    :    :    :    :    :    :    :    :    :
Db	62	VDHNVSTSPERKF-----IKNEESRIQVEALAKAKAFGVEYYSENDIRQGIHVHIIG 116
		:    :    :    :    :    :    :    :    :    :    :    :    :
Qy	126	EQGFTLPGTTWCSDSHSTHGAFALAFGIGTSVEHVLATQCLITKRSKNMRIODGE 185
		:    :    :    :    :    :    :    :    :    :    :    :    :
Db	117	EQGFTLPGMTIVCGDSHTSTHGAFALAHGIGTSVEHVLATQTILQRKAKNMLVRVDGQ 176
		:    :    :    :    :    :    :    :    :    :    :    :    :
Qy	186	LAPGVSKDVLLHAIGIITAGTGAVIEPCGSVIISLSWEARMSICNNMSIEGGARAGW 245
		:    :    :    :    :    :    :    :    :    :    :    :    :
Db	177	LPEGVTAKDIILAIIGBIGTAGTGVIYEAGEAIRSLSEMGRTMCNNMSIEGGARAGLI 236
		:    :    :    :    :    :    :    :    :    :    :    :    :
Qy	246	APDEITEPYLKGRPLAPKYDSPWHKATOVWKNLQSDPGAKYDIDVFIDAKOIVPTLTWG 305
		:    :    :    :    :    :    :    :    :    :    :    :    :
Db	237	ADETTFAYVKDKRPAPK--GAAWDAALAAYKWTLQSDGEGAHFDKVLVDAAKLPPIVSWG 294
		:    :    :    :    :    :    :    :    :    :    :    :    :
Qy	306	TSPEDVVPIITGVVPDPETFAATEAKADGRRMLQYMGLKAGTGMEDIPVDKVFIGSGTNSR 365
		:    :    :    :    :    :    :    :    :    :    :    :    :
Db	295	SSPEDVVSVQGVVNPPEEITDENKRTSKIRALDYMGLTPGTKITDALDRVFIGSGTCNGR 354
		:    :    :    :    :    :    :    :    :    :    :    :    :
Qy	366	IIDLRAAAVVKRKKAPVKSAMVPGSLVKVTAEEGLDKIFPEAGFEFWREACSCMC 425
		:    :    :    :    :    :    :    :    :    :    :    :    :
Db	355	IIDLRAAAKVIIEGKTNPVR-NAMIVPGSLVKVEQAEGLDKIFLAFGDFWRPEGCSCMC 413
		:    :    :    :    :    :    :    :    :    :    :    :    :
Qy	426	LGNVPDTLAPQERCASNTSNRPFEGOGAGRTHLMSPVMAAAAGIVGKLADYVKLTDDYK 484
		:    :    :    :    :    :    :    :    :    :    :    :    :
Db	414	LANNDLKPKHERCASTSNRPFEGOGFKGRTHLVSPAAAAAAAIAIGHFVDIR---DWK 469
		:    :    :    :    :    :    :    :    :    :    :    :    :

  

RESULT 6	
Q9EV53	ID Q9EV53 PRELIMINARY; PRT; 448 AA.
AC	Q9EV53;
CD	Q9EV53;
DT	01-MAR-2001 (TrEMBLrel. 16, Created)
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE	2-isopropylmalate isomerase large subunit (Fragment).
GN	LEUC.
OS	Rhizobium melloti (Sinorhizobium meliloti).
OC	Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC	Rhizobiaceae; Sinorhizobium.
OX	NCBI_TaxID=382;
ON	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=GR4.
RA	Sanjuan-Pinilla J.M., Munoz S., Olivares J., Sanjuan J.;
RT	"The Sinorhizobium meliloti leuA gene is essential for symbiosis.";
RT	submitted (OCT-2000) to the EMBL/GenBank/DBP databases

DR EMBL; AJ296268; CAC14578.1; -.  
 DR InterPro; IPR001030; Aconitase\_N.  
 DR InterPro; IPR004430; Leuc.  
 DR Pfam; PF00330; aconitase; 1.  
 DR PRINTS; PR00415; ACONITASE\_N.1.  
 DR ProDom; PD000511; Aconitase\_N.1.  
 DR TIGRFAMs; TIGR00170; leuc; 1.  
 DR PROSITE; PS00450; ACONITASE\_1; 1.  
 DR PROSITE; PS01244; ACONITASE\_2; UNKNOWN\_1.  
 DR Isomerase.  
 KW NON\_TER  
 FT SEQUENCE 448 AA; 48466 MW; 029B65EA51A054BD CRC64;  
 SQ  
 Query Match 38.5%; Score 1563; DB 2; Length 448;  
 Best Local Similarity 66.1%; Pred. No. 2.6e-97;  
 Matches 300; Conservative 53; Mismatches 93; Indels 8; Gaps 3;  
 QY 26 DGVLYLYDRHLVHEVTSPOAFEGLRNAGKRVRRPDCLTATTDHNVPTTSRKALKDIASF 85  
 DB 1 DGTCLLYDCHLVHEVTSPOAFEGLRNAGKRVRRPDCLTATTDHNVPTTSRKALKDIASF 55  
 QY 86 IKEDDSRTQCVTLLENVKEFGVTEGLSDKRGIVHVIQPEGGFTLPPTVVCSDSHST 145  
 DB 56 IKNESRIQVEALRNADLGEVETSENDKRGIVHVIQPEGGFTLPPTVVCSDSHST 115  
 QY 146 HGAFGALAFGIGTSEVEHVLATQCLITRKSNNRQVDEGLAPGVSSKQVLAHAIIGT 205  
 DB 116 HGAGGALAHGIGTSEVEHVLATQCLITRKSNNRQVDEGLAPGVSSKQVLAHAIIGT 175  
 QY 206 AGGTGAVIEFGSVIRSLSMERNSICMSIEGARGAVAPDETTEFYLKRPAPKYD 265  
 DB 176 AGGTGAVIEFGSVIRSLSMERNSICMSIEGARGAVAPDETTEFYLKRPAPKYD 235  
 QY 266 SPEHKAATQYKKNLOSDBGAKYDIDVFIADKIIVPLTMTGSPEDVVPITGVPPETFA 325  
 DB 236 A-MDRAVEYKTLHMDGAYDVRVLDANLPPIVSGSSPELVVSVQGVNPPDIQ 293  
 QY 326 TEAKKADGRMLQYVGLKAGTPEMDIPVDKVFISGCTNSRIEDLRAAAAYVGRKKAPV 385  
 DB 294 DETRTSKMRALDVGGLRPGTKITDIAIDRVIGSCTNGRIEDLRAAAAYVGRKKAPV 353  
 QY 386 KSANVPPSGLVYTOAEEBGLDKITEFGKFEWREAGSCMLGMNDIAPORCASTSR 445  
 DB 354 -SAMIVPSSGLVKEQAEABGLDKIFEAGFDWREPGSCMLGMNDIAPORCASTSR 412  
 QY 446 NEEGROGAGRTHLMSPVMAAAGIVGKLADVRX 479  
 DB 413 NEEGRQGFGRTHLSPMAAAVAAGHFVDIRE 446  
 RESULT 7  
 Q9ABNO PRELIMINARY; PRT; 479 AA.  
 AC Q9ABNO; 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DN 3-isopropylmalate dehydratase, large subunit.  
 GN CC0196.  
 OS Caulobacter crescentus.  
 OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;  
 CC Caulobacter.  
 NCBI\_TaxID=155892;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 19089 / CB15;  
 MEDLINE=21173698; PubMed=11259647;  
 RA Eisen J., Heidelberg J.F., Laub M.T., Paulsen I.T., Nelson K.E.,  
 RA Poczocki I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,  
 RA Deboy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,  
 RA Kolonay J.F., Smit K., Craven M.B., Khouri H., Shetty J., Berry K.,  
 RA Uitterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,

RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;  
 RT "Complete genome sequence of *Caulobacter crescentus*."  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).  
 DR EMBL; AE005694; AAK22183.1; -.  
 DR TIGR; CC0196; -.  
 DR InterPro; IPR001030; Aconitase\_N.  
 DR InterPro; IPR004430; Leuc.  
 DR Pfam; PF00330; aconitase; 1.  
 DR PRINTS; PR00415; ACONITASE.  
 DR ProDom; PD000511; Aconitase\_N.1.  
 DR TIGRFAMs; TIGR00170; leuc; 1.  
 DR PROSITE; PS00450; ACONITASE\_1; 1.  
 DR PROSITE; PS01244; ACONITASE\_2; UNKNOWN\_1.  
 DR Complete proteome.  
 KW SEQUENCE 479 AA; 50693 MW; BE19EB931A251BFA CRC64;  
 SQ  
 Query Match 38.5%; Score 1562; DB 16; Length 479;  
 Best Local Similarity 64.4%; Pred. No. 3.3e-97;  
 Matches 307; Conservative 53; Mismatches 105; Indels 12; Gaps 5;  
 QY 9 QLYYDKVLYQAHVVDKLDGTVLYLYDRHLVHEVTSPOAFEGLRNAGKRVRRPDCLTATTD 68  
 DB 4 KTVYDKIWDAAVVS-AGGEALIVYDHLIHEVTPQAFGLRAAGKRVRRPDCLTAVAD 62  
 QY 69 HNVPTTSRKALKDIASFTEKEDSRTQCVTLLENVKEFGVTEGLSDKRGIVHVIQPEGG 128  
 DB 63 HNIPEGALGVDA--VADEARLQLTLARNVADNIEFPMDGINNGIVHVIQPEGG 119  
 QY 129 FTLPGTAVCGDSHTSTGAFGALAFGIGTSEVEHVLATQCLITRKSNNRQVDEGLAP 188  
 DB 120 RTQPGMTIVCGDSHTSTGAFGALAHGIGTSEVEHVLATQCLITRKSNNRQVDEGLAP 179  
 QY 169 GVSSKQVLAHAIIGTGTGAVIEFGSVIRSLSMERNSICMSIEGARGAVAPDETTEFY 248  
 DB 180 GVTGKQVALAVYIEGIGTGTGAVIEFGSVIRSLSMERNSICMSIEGARGAVAPDETTEFY 239  
 QY 249 EITFEYLKRPAPKYDPEHKAATQYKKNLOSDBGAKYDIDVFIADKIIVPLTMTGSP 308  
 DB 240 DKTFAVIGKPPAPK--GAAMDALSHWKTFTTDDAVFDRTVIDGSLVPMVTWGTSP 297  
 QY 309 EDVVPITGVPPETFEAKKADGRMLQYVGLKAGTPEMDIPVDKVFISGCTNSRIED 368  
 DB 298 EDVIVTGVNPPESFAIPDRAAHRALDVMGLKAGPISARIDRVIGSCTNSRIED 357  
 QY 369 LRAAAAYV-----GRKAPNVKSAVVPGSLVYTOAEEBGLDKITEFGKFEWREAGS 423  
 DB 358 MRAAAAYVQEAFLHGRVLAAPHV-K-AMVVPSSGLVKEQAEABEGLDAIFRAAGDFDWRP 416  
 QY 424 MCLGMNDIAPORCASTSRNNEFGROGAGRTHLMSPVMAAAGIVGKLADVRK 480  
 DB 417 MCLAMNPDLAPORCASTSRNNEFGROGAGRTHLMSPVMAAAGIVGKLADVRK 473  
 RESULT 8  
 Q9JZT5 PRELIMINARY; PRT; 469 AA.  
 AC Q9JZT5; 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DN 3-isopropylmalate dehydratase, large subunit.  
 GN NMB1036.  
 OS Neisseria meningitidis (serogroup B).  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 NCBI\_TaxID=491;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MC58 / SEROGROUP B;  
 MEDLINE=20175755; PubMed=10710307;  
 RA Teddlin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,  
 RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,  
 RA Nelson W.C., Gwinn M.L., Deboy R., Peterson J.D., Hickey B.K.,  
 RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,

RX	MEDLINE=2022256; PubMed=10761919;
RA	Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA	Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA	Davies R.M., Davis P., Devlin K., Fellwell T., Hamlin N., Holroyd S.
RA	Jagels K., Leather S., Moule S., Wungall K., Quail M.A.,
RA	Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA	Whithead S., Spratt B.G., Barrrell B.G.;
RT	"Complete DNA sequence of a serogroup A strain of Neisseria
RL	meningitidis Z2491.";
RL	Nature 404:502-506(2000).
DR	ENBL; ALI62756; CAB84686.1; -;
DR	InterPro; IPR001030; Aconitase_N.
DR	InterPro; IPR004430; LeuC.
DR	Fram; PF00330; aconitase; 1.
DR	-PRINTS; PR00415; ACONITASE.
DR	PRODOM; PD00511; Aconitase N; 1.
DR	TIGRFAMS; TIGR00170; leuc; 1.
DR	PROSITE; PS00450; ACONITASE_1; 1.
DR	PROSITE; PS01244; ACONITASE_2; 1.
KW	Lysate; Complete proteome.
SQ	SEQUENCE 469 AA; 50783 MW; 89AE349827DA35DB CRC64;
	Query Match 38.1%; Score 1545.5; DB 16; Length 469;
	Best Local Similarity 63.4%; Pred.No. 4.2e-96;
	Matches 301; Conservative 62; Mismatches 103; Indels 9; Gaps
QY	7 TPQTLYDKVLQAHVDEKLDGTVLLYIDRHLEVHVSPOAFGLRNAGRKVRPDCDTLAT 66       :    :
Db	2 TAQTLVDKLNSHWREEDGTVLLYIDRHLEVHVSPOAFGLKNAGRISDVSVST 61       :    :
QY	7 TDHNVTTSRKALKDITASFTFKDDSDTCQCIVTEENVKEFG-VTYFGLSKDROGVHHVIP 125       :    :
Db	62 ADHTPT-----GDWDKIQDPISKLVDTLTKNKEFGALAYFFPDMDGGIVHVMGP 115       :    :
QY	126 EQGFTLP GTT VWCDSHT THGA FGAL AFGI GTSEV EHV L AT QCL IT KR SKNM RI Q VDGE 185       :    :
Db	116 EQGAT LPGM TVCDS HTTH GA FGALA HGI GT SEVE HTMA QTCA KKSKMLIAVD GK 175       :    :
QY	186 LAPGSVK DVVLA HI GI TAGTGTA VI EF CG SVIRSL SWEARMSICNW SI EG GAR AGNV 245       :    :
Db	176 LKA GV TAKD VAL YII GOI TAG TG TGYA IFEGEAI RLSMEGRMTLCNNM AI EAGA RS GMV 235       :    :
QY	246 APDEIT FEYLKG RLAPKY DSPWHKATQYNKKNLQS DP CA KY DI DV IDAKDI VP LT TWG 305       :    :
Db	236 AVDT TT DY VKDF PAPEEA-- WD KA VEYWR TL VS DE GA VF DK EV RFNA ED IE Q VTWG 293       :    :
QY	306 TSDEDVP ITGVV DD ET FATE NKAD GRMI QYW GL KA GT WMEDI PV DKVF IG SCT NSR 365       :    :
Db	294 TSP EW LD IS SKYP AEET PD PKRS GM FRAL EYMGLEAGT FLNE IPDVIF IGSC TN SR 353       :    :
QY	366 IEDLR AAAAV KG RKAPA NVKS AMVVPG SLVK TOABEE BL DK IFEA GFWE RGCSMC 425       :    :
Db	354 VED LR EAAL AK DR KA AN QR VL IV PG SSL VK EOAE KEGL DK IFEA GF WE RG CS MC 413       :    :
QY	426 LGNP DI LA PQ ER CAST SN RN FEGRQG AGRR TH LM SP VNAAAAG I VG KLAD VRKL 480       :    :
Db	414 LANVA DLTPGOR CASTSNRN FEGRGN CR TH LVSPA MAAAAAA VTGF RTD IRMM 468       :    :



RP		SEQUENCE FROM N.A.
RC	STRAIN=ATCC_15692 / PAOI;	
RX	MEDLINE=20437337; PubMed=10984043;	
RA	Stover C.K., Plasm X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,	
RA	Hickey M.J., Birkman F.S.L., Hutnagle W.O., Kowalik D.J., Lagrou M.,	
RA	Gaber R.L., Goltzy L., Tolentino E., Westbrook-Madigan S., Yuan Y.,	
RA	Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbidgen K., Lim R.M.,	
RA	Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,	
RA	Reizer J., Seier M.H., Hancock R.E.W., Lory S., Olson M.V.;	
RT	"Complete genome sequence of Pseudomonas aeruginosa PAOI, an	
RT	opportunistic pathogen." ;	
RL	Nature 406:959-964(2000).	
DR	EMBL: AE004736; AACG6509.1; -	
DR	InterPro: IPRO01030; Aconitase_N.	
DR	InterPro: IPR00430; Leuc.	
DR	Pfam: PF00330; aconitase; 1.	
DR	PRINTS: PR00415; ACNITASE.	
DR	ProDom: PD000511; Aconitase_N; 1.	
DR	TIGRFAMs: TIGR00170; leuc; 1.	
DR	PROSITE: PS00450; ACNITASE_1; 1.	
DR	PROSITE: PS01244; ACNITASE_2; 1.	
KM	Complete proteome.	
SQ	SEQUENCE 474 AA; 51042 MM; 7B4A0F6500C228EC CRC64;	
Query Match	37.2%; Score 1507.5; DB 16; Length 474;	
Best Local Similarity	62.5%, Pred. No. 1.6e-93;	
Matches 295; Conservative	61; Mismatches 113; Indels 3; Gaps	2.
QY	9 OTLVKVCQAHVVDKLGTGLVLYTDRIHNVHTSPFAEFGRLRNAGRKRRPDDCTATTD 68	
Db	4 KTLVTKLMDMLVKQRDDSLALITYIDRHILHEVTSPFAEGRLAKGRKKWRIDANINATPD 63	
QY	69 HNVPTTSRKALKDIASFIKEDDSRTQCVTLENNVKEFGVTYFGSLDKRGIVHYVGPEQG 128	
Db	64 HNVPTTRTERKKGIIAA-TADEVSRLQOVLTLDENCDDFGITFEKMADVROGIYHVAVGPEQG 122	
QY	129 FTLPETTVCGSHNSTIGAIFAGLAFGICSTSEVENHLAQCLITRSKNMRLOYGSELAP 188	
Db	123 ATLPMFTVTCGSHSTHGAFGLAHGIGTSEVENHLAQCLVAKMKRMVLKVEGRFLPA 182	
QY	189 GVSSKDQVYLHAIGIIGTAGTGAVIEFCGSVIRLSJMEARMSICNMISBGARAGAVAD 248	
Db	183 CVTAADIYLAIVAGRIGTAGNGHAIIEFPASAIRDLISBERMTICNMISAGARVGLAAD 242	
QY	249 EITFEYLGKRPLAPKYSDSEWHKATQYWKNLQSDPGAKYDIDVFIDAKDIVPLTWGTSF 308	
Db	243 QKITDYVKGSRPAP--SABQMDOAVACWCGVLSADADARFDVTVELDAQIKPVWSGTSF 300	
QY	309 EDVVITGVDPPEPFATKAADGRRLQYWGKLKAGTMEDIPVDKVITIGSTNSRID 368	
Db	301 EMVLAVDVONVPDPAESDPIKRGSIERALKVMGLRFNQAITIDLRVFIGSTNSRID 360	
QY	369 LRAAAAYVGRKARPVKSAVVPPSGVLKTQAEPEGGLKIIFEEBAEFEREAGCSNCLGM 428	
Db	361 LRAAAEVARGRVYAATIKALIVPSSGLVKEQAEKGLDIRIFIENGFERREPOCSSCLLM 420	
QY	429 NPDI LAPERCASSTSNRNFEGROGAGGRTHLMSPVMAAAAAGIVGKLADVRKL 480	
Db	421 NPDRLESQHCAKSTSNRNFEGROGAGGRTHLVSPAAAAAAAYVAGRIDVRKL 472	
RESULT 11		
O9PAXO		
ID O9PAX0:	PRELIMINARY;	PRT; 474 AA.
AC O9PAX0:		
DT 01-OCT-2000 (TREMBLrel. 15, Created)		
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)		
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)		
DE 3-isopropylmalate dehydrogenase large subunit.		
GN XF2375.		
OS Xylella fastidiosa.		
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;		
Xylella.		

[1]

```
RN NCB1_TaxID=371;
RP SEQUENCE FROM N.A.
RC STRAIN=9A5C;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach P.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvaranga R., Alves L.M.C., Araya J.E., Bata G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carter H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.P., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Facchini A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furian L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Honneisel J.D., Junqueira M.L., Kemper E.L., Kietajna J.P.,
RA Krueger J.E., Kuramae E.B., Laigret F., Lambais M.R., Leite J.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Martino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsumura A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Neto L.E.S.,
RA Nhani A., Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A., Jr., Pesquero J.B.,
RA Quagrio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E., Jr., de Sa R.G., Sartelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A., Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Siquela W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuchino M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis V., Seubal U.C.;
RT "the genome sequence of the plant pathogen Xylella fastidiosa,"
RL Nature 406:151-159(2000).
DR EMBL; AE004047; AF85174.1; -.
DR InterPro; IPR001030; Aconitase_N.
DR InterPro; IPR004430; LeucP.
DR Pfam; PF00330; aconitase; 1.
DR PRINTS; PR00415; ACONITASE.
DR Prodom; PD000511; Aconitase_N_1.
DR TIGRFAMs; TIGR00170; leuc; 1.
DR PROSITE; PS00450; ACONITASE_1; 1.
DR PROSITE; PS01244; ACONITASE_2; 1.
KW Complete proteome.
SQ
SEQUENCE 474 AA; 51183 MW; 998D5FD82B23750 CRC64;

Query Match          37.0%; Score 1498.5; DB 16; Length 474;
Best Local Similarity 63.1%; Pred. No. 6.4e-93;
Matches 298; Conservative 52; Mismatches 119; Indels      3; Gaps      2;
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QY 369 LRAAAVVKRKKAPNVKSNMVPVPGSLVKTQAEELGDKIFEBAGFEWREAGCSMCLGM 428
D 361 LRAAAEVVKRKKVASTVQKQMVVPGSLVKAQAEVEGLDKIFEBAGFEWREPGCSMCLAM 420
QY 429 NPDLAPQBERCASTSNRNFEGRGAGGRTHLMSVPMVMAAAAGIVGKLADVRKL 480
D 421 NPKJSGEHCASSTSNRNFEGRGIGGRTHLVSPAMAAAAAAGVDFVDVREM 472

RESULT 12
Q8XXX3 PRELIMINARY; PRT; 469 AA.
AC Q8XXX3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Probable 3-isopropylmalate dehydratase (Large subunit) protein
DE (EC 4.2.1.33).
GN LEUC OR RSC1990 OR RS03558.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
OC Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler C., Choisme N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Sigulier P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL; AL646067; CAD15692.1; -.
DR InterPro; IPR001030; Aconitase_N.
DR Pfam; PF00330; aconitase; 1.
DR PRINTS; PR00415; ACONITASE.
DR PRODOM; PD000511; Aconitase_N; 1.
DR TIGRFS; TIGR00170; leuc; 1.
DR PROSITE; PS00450; ACONITASE_1; 1.
DR PROSITE; PS01244; ACONITASE_2; 1.
KW Lyase; Complete proteome.
SQ SEQUENCE 469 AA; 50796 MW; B451E96E44788AAE CRC64;

Query Match 36.8%; Score 1493; DB 16; Length 469;
Best Local Similarity 63.5%; Pred. No. 1.5e-92;
Matches 301; Conservative 53; Mismatches 110; Indels 10; Gaps 3;

QY 9 QTLVDKVLQAHVDEKLDGTLLYIDRLHVEVTSPOAFEGRLNAGRKVRPDCCTLATTD 68
D 3 KTLVDKLDHVVHTEDGTLLYIDRLHVEVTSPOAFEGRLNAGRKVRPWRISANLAVSD 62
QY 69 HNVPTTSRKALKDIASFIKEDDSRTQCVTLLENVKEFGVTFYGLSKRQGIHVHIGPEQG 128
D 63 HNVPTTDR-----SHGIADPVSKLOVDLTLDNCDSFGITQFKMTDKRQGIHVHIGPEQG 116
QY 129 FTLPGETTVVCGDSHTSTHGAFALAFGIGTSEVHVLATQCLITKRSKNMRIQVDGELAP 188
D 117 ATLPGETTVVCGDSHTSTHGAFALAFGIGTSEVHVLATQCLITKRSKNMRIQVDGELAP 176
QY 189 GVSXKDVVLHAIGITAGGTGAVIEPCGVIRSLSEARMSICNMSIEGGRAGMVPAD 248
D 177 GCTAKDIVLAIIGKITAGGTGAVIEPCGVIRSLSEARMSICNMSIEGGRAGMVGVD 236
QY 249 EITFEYKGRPLAPKDYDSEPHKATQWKNLQSDPGAKYDIDVFIDAKDVIPTLTWTGTS 308
D 237 DITLEYIKGRPPAPQ--GVMEQAVAYWRSLSHSDGARFHDVHVELRAEIRPQVSWGTSP 294
QY 309 EDVVPITGVVDPDETATEKAKDGRNLMQYMGKAKTGMEDIPVDKVFVGTGSCNRSIED 368
D 309 EDVVPITGVVDPDETATEKAKDGRNLMQYMGKAKTGMEDIPVDKVFVGTGSCNRSIED 368
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D 235 EMVTSIEDRVDPDKEDPDKENAMERALEYVALQPNVAIGDIRIDKIVFGSCNRSIED 354
QY 369 LRAAAAVVK--GRKKAPNVKSNMVPVPGSLVKTQAEELGDKIFEBAGFEWREAGCSMCL 426
D 361 LRAAAEVVKRKKVASTVQKQMVVPGSLVKAQAEVEGLDKIFEBAGFEWREPGCSMCL 420
QY 429 NPDLAPQBERCASTSNRNFEGRGAGGRTHLMSVPMVMAAAAGIVGKLADVRKL 480
D 421 NPKJSGEHCASSTSNRNFEGRGIGGRTHLVSPAMAAAAAAGVDFVDVREM 472
D 415 AMNADRLPEFGERCASTSNRNFEGRGAGGRTHLVSPAMAAAAAAGVDFVDVREM 468
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## RESULT 13

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Q8XXA00 PRELIMINARY; PRT; 466 AA.
ID Q8XXA00;
AC Q8XXA00;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 3-Isopropylmalate isomerase (dehydratase) subunit.
DE LEUC OR Z0081 OR ECS0076.
GN Escherichia coli O157:H7.
OS Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfal G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Rodabaugh J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca E.J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,
RA Kihara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
DR EMBL; AE005184; AGS4376.1; -.
DR EMBL; AP002550; BAB33499.1; -.
DR InterPro; IPR001030; Aconitase_N.
DR InterPro; IPR004430; Leuc.
DR Pfam; PF00330; aconitase; 1.
DR PRINTS; PR00415; ACONITASE.
DR PRODOM; PD000511; Aconitase_N; 1.
DR TIGRFS; TIGR00170; leuc; 1.
DR PROSITE; PS00450; ACONITASE_1; 1.
DR PROSITE; PS01244; ACONITASE_2; 1.
KW Isomerase; Complete proteome.
SQ SEQUENCE 466 AA; 49898 MW; 4722550F4C7772EA CRC64;
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Query Match 36.2%; Score 1469.5; DB 16; Length 466;  
Best Local Similarity 61.9%; Pred. No. 5.6e-91;  
Matches 292; Conservative 59; Mismatches 112; Indels 9; Gaps 4;

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QY 9 QTLVDKVLQAHVDEKLDGTLLYIDRLHVEVTSPOAFEGRLNAGRKVRPDCCTLATTD 68
D 3 KTLVDKLDHVVHTEDGTLLYIDRLHVEVTSPOAFEGRLNAGRKVRPQKGTATMD 62
QY 69 HNVPTTSRKALKDIASFIKEDDSRTQCVTLLENVKEFGVTFYGLSKRQGIHVHIGPEQG 128
D 63 HNVSTQT---KDNAC--GEWARIQMQLIKNCFGVGLYDLNHPYQGIHVHVGPEQG 116
QY 129 FTLPGETTVVCGDSHTSTHGAFALAFGIGTSEVHVLATQCLITKRSKNMRIQVDGELAP 188
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```
Db 117 VTLGCMITVCGDSHTATGAFGALAFGIGTSEVEHVLTATQTLKQGRATMKIEVGGKAP 176
Qy 189 GVSSADVVAHAIIGTGTGAVIEFCGSVIRSLSEARNISICNMSIEGARAVMPD 248
Db 177 GITAKDIYALAIIGKTGSAGTGCHVIEFCGEAIRDLSMEGRMLCNMALEMGAAGLVAPD 236
Qy 249 EITFEYLKGRPLAPKYDSEPMHKATQYWKNIQSDPAKYDIDVFIDAKDIYVTLTWGTS 308
Db 237 ETTFNVYVGRHLAPK--GKDFDAVAWYMTLQTDGATFDFTVTLQABEISPOYWTGNP 294
Qy 309 EDVVPITGVVDEPFEIATKADGRMLQYWGGLAGTPEMEIIPVDKXIFIGCTSRIED 368
Db 295 GQVIVSVDNIDPSPAFADPVERASAEKALAYWGLKPGILTEVALDKVFIIGSCTSRIED 354
Qy 369 LRAAAVAVKGRKKAPNVASAMVPGSGLVKTOAESEGLDKIPEEAGFEWREAGSMCLGM 428
Db 355 LRAAAEIKKGRKVAFGVQ-ALVVPSSGPVKAQAEAGLDKFIIEAGFEWRLPGCSMCLAM 413
Qy 429 NPDLAPQERCASTSNRNFEGROGAGRTHLMSPVMAAAGIVGLADYVKL 480
Db 414 NNDLNPBERCASTSNRNFEGROGGRTHLVSPMAAAAATGTFADIRNI 465

RESULT 14
Q8ZIH0 PRELIMINARY; PRT; 476 AA.
AC Q8ZIH0:
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE 3-Isopropylmalate dehydratase large subunit (EC 4.2.1.33).
GN LEUC OR YPO0531.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Yersinia.
OC NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / BIOVAR ORIENTALIS;
RX MEDLINE=21470413; PubMed=11586360;
RA Pakhilli U., Wren B.W., Thomson N.R., Tiltball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Baaham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltham T., Hamlin N., Holroyd S., Jagsels K., Kariyasev A.V.,
RA Leather S., Mouton S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrett B.G.,
RA "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
DR EMBL: AJ141413; CAC89388.1; -.
DR InterPro: IPR001030; Aconitase_N.
DR InterPro: IPR004430; Leuc.
DR Pfam: PF00330; aconitase; 1.
DR PRINTS: PR00415; ACONITASE.
DR PRODOM: PD000511; Aconitase_N; 1.
DR TIGRFAMs: TIGR00170; leuc; 1.
DR PROSITE: PS00450; ACONITASE_1; 1.
DR PROSITE: PS01244; ACONITASE_2; 1.
DR Lysase; Complete proteome.
SQ SEQUENCE 476 AA; 50589 MW; 052D8ED2165E5E74 CRC64;

Query Match 35.8%; Score 1452; DB 16; Length 476;
Best Local Similarity 59.2%; Pred. No. 8,9e-90;
Matches 289; Conservative 66; Mismatches 121; Indels 12; Gaps 5;
```

```
Qy 121 HVIEGEGFTLPETTVCGDSTHTGAFGALAFGIGTSEVEHVLTATQCLTKSKMNI 180
Db 115 HVIEGEGMTLPGMTIVCGDSHTATGAFGSLAFGIGTSEVEHVLTATQTLKQGRKTR 174
Qy 181 QYDGEIAPGVSSKDVVAHAIIGTGTGAVIEFCGSVIRSLSEARNISICNMSIEGGA 240
Db 175 EVNGTVGAGITAKDVLAIIGKTGSAGTGCHVIEFCGEAIRDLSMEGRMLCNMALEMGA 234
Qy 241 RAGVAPDEITFEYLKGRPLAPKYDSEPMHKATQYWKNIQSDPAKYDIDVFIDAKDI 300
Db 235 KAGLVAPDDITFAVYKQGQFAP--TGEQMEGVAVWRLTKSDADQFPTIYTLDAADIA 292
Qy 301 TLTWGTSEDEVPIITGVVDPETPATKADGRMLQYWGGLAGTPEMEIIPVDKXIFIG 360
Db 293 QVTWGTNGQYIAVAVQIIPAESEFSDPVERASAEKALAYMDLPGIKLTEVALDKVFI 352
Qy 361 CTNSRIEDLRAAAAVKGRKKAPNVASAMVPGSGLVKTOAESEGLDKIPEEAGFEW 420
Db 353 CTNSRIEDLRAAAALAQGRKVAQVQ-ALVVPSSGPVKAQAEAGLDKFIIEAGFEW 411
Qy 421 GCSMCLGNPDILAPQERCASTSNRNFEGROGAGRTHLMSPVMAAAGIVGLADYVKL 480
Db 412 GCSMCLANNDRLEBERCASTSNRNFEGROGGRTHLVSPMAAAAATGTFADIRNI 471
Qy 481 TDYKASPH 488
Db 472 S---ATTH 476
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## RESULT 15

Q9KP81 PRELIMINARY; PRT; 467 AA.

```
AC Q9KP81:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE 3-Isopropylmalate dehydratase, large subunit.
GN VC2492.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OC NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EL TOR N1691 / SEROTYPE O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RL Nature 406:477-483(2000).
DR EMBL: AE004318; AAP95634.1; -.
DR TIGR: VC2492; -.
DR InterPro: IPR001030; Aconitase_N.
DR InterPro: IPR004430; Leuc.
DR Pfam: PF00330; aconitase; 1.
DR PRINTS: PR00415; ACONITASE.
DR PRODOM: PD000511; Aconitase_N; 1.
DR TIGRFAMs: TIGR00170; leuc; 1.
DR PROSITE: PS00450; ACONITASE_1; 1.
DR PROSITE: PS01244; ACONITASE_2; 1.
DR Complete proteome.
SQ SEQUENCE 467 AA; 50185 MW; 4F7607148FA85ADD CRC64;
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Query Match 35.2%; Score 1425.5; DB 16; Length 467;
Best Local Similarity 58.9%; Pred. No. 5.3e-88;
Matches 279; Conservative 67; Mismatches 119; Indels 9; Gaps 4;
```



Query Match	Best Local Similarity	Score	DB 2	Length	466
Matches 268; Conservative 74; Mismatches 121; Indels 9; Gaps	56.8%;	Pred. No. 3.3e-83;			
9	OTLYKRVUAAHVDEKLDGTVLLYIDRLVHVHTSPQAFEGRLNAGKVRBPDCTLATD	68			
3	KTLVYKRIYDSHVHSEKNGSLTYVDLHLHLEHTVSPQAFESLRIDRYRQKKTFFATMD	62			
69	HNVPTTSRKALADIASFIKEDDSRTQCVTLLENVVEFGVYFGSLDKRQGIHVHIGPEGG	128			
63	HNVHSE-----KDINA--SGSMAKIQMOGLINCKCEFHISLYDLNHPNOGIHVHISPEQG	116			
129	FLLPCTTVCGDSHTSSTHGAFGALAFGIGTSEVENYLAQCLITRSKMRLOVDSGLAP	188			
117	MTLPGVAVICGDSHTSHTGAFGALFEGIGTSEVENYLAQCLITRQKQKFKMKLEVIKIGN	176			
189	GVSSKQVVAHAGIIGTAGTGAVIEFCGSAVRSLSMEARMSICNMSIEGARAGAVAPD	248			
177	FTTADVLIYITIGKIGSSAGCTGIIEFCGNVKKMSMERMTVCNNAIELGAKSGLIAD	236			
249	EITFEYLKGRPLAPKYDSEPMHKAQYWKNLQSDPEAKTIDIVFIKAKIIVPLTGTSP	308			
237	ETTYLTKKKTSP--HGNMQKALIEYWKTLTKTDHNAIPDKVFTTIDISILPQVWTGNP	294			
309	EDVVPITGVVPEETFAATBAKKADGRMLQYMGILKGTPEMEDIIVDKVIFGCTNSRIED	368			
295	DQYIGINEKIPDSTSQNIYKDKLAKSACKMDLKGYITIDITDKVIFGCTNSRIED	354			
369	LRAAAIVVKGKKAPNVKSMVVGSGLVKTOAEEGLDKIFEAGFENWEACSGMCLM	428			
355	LRASAKILHNKNIKSKNVK-ALVVGSGLVKROAESGLDKIFEAGFEMWLPFGCSMCLM	413			
429	NPDILAPQERCASTSVNRFEGROGAGRTILMPPWMAAAAGIYGLADYKL	480			
414	NNDRLESENRCASTSNRNFEGROGRNGRTHLVSPVIAALALYGFSPNPKL	465			

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DR InterPro; IPR001030; Aconitase_N.
DR InterPro; IPR004430; LeuC.
DR Pfam; PF00330; aconitase; 1.
DR PRINTS; PR00415; ACONITASE.
DR ProDom; PD000511; Aconitase_N; 1.
DR TIGRfams; TIGR00170; leuC_1.
DR PROSITE; PS00415; ACONITASE_1; 1.
DR TIGRfams; TIGR00170; leuC_1.
DR PROSITE; PS00450; ACONITASE_1; 1.
DR PROSITE; PS01244; ACONITASE_2; 1.
DR isomerase; Plasmid.
KW NON TER 448 448
SQ SEQUENCE 469 AA; 52426 MW; 4094EC232646228B CRC64;

Query Match 33.4%; Score 1354; DB 2; Length 469;
Best Local Similarity 56.6%; Pred. No. 3.6e-83;
Matches 267; Conservative 76; Mismatches 119; Indels 10; Gaps 5;

QY 9 QTLVDKVLQAHVDEKLDGTLLYIDRHLVHEVTSPOAFEGRLNAGRKVRPDCDTLATTD 68
DB 3 KTLVEKIYDAHIVHEEKNISILYIDLHLVHEVTSPOAFDSLWRNRSVRQPKTFTAMD 62
QY 69 HNVPTTSRKALKDIASFTEKEDDSTQCVTLLENVKEFGVTFGLSDRQGIHVHVGPEQG 128
DB 63 HNVSTES----KDINA--SGSMAKIQMQLIKNCEEFNIALYDLNPNKQGIHVHVGPEQG 116
QY 129 FTLPGTTVCGDSTHTHGAFALFGIGTSEVHVLATQCLITKRSKNMRIQVDGELAP 188
DB 117 LTLPGSTIVCGDSTHTHGAFALSGFGIGTSEVHVLVDTQLKQORFKNMKIKVGVKK 176
QY 189 GVSKDVLVHLAIGITAGGTGAVIEFCGVSIRSLSEARMSICNMSIEGGARAGVAPD 248
DB 177 FITAKDILFTIGKLGTSFGVIEFCGVDIKONNEERTICNMALEMGAKSALLAPD 236
QY 249 EITEYLLKGRPLAPKYDSEPHKATQYWKQLQSDPGAKYDIDVIDAKDIVPTLTWTGSP 308
DB 237 ETTLYLLKNKRYSPK--NKYWDISAIRYKLTVDENALDFKEFTDISDPSQVWTGSP 294
QY 309 EDVVPITGVVPDPTFATEAKKADGRMLQYMGKAGTPEMEDI PVDKVFISGCTNSRIED 368
DB 295 DQVLSINEKIPDNFSFKDSIKDLARSACNYMDLKPSYLNKIKDKVFGISCTNSRIED 354
QY 369 LRAAAAVVGRKKAPNVKSAWVPGSLVKTQAEELGDKIFEBAGFEWREAGSCMLGM 428
DB 355 LRSAAATLLKNKTSKNIK-AIIVPGSGSVKNQAEKEGLDKIFIDAGFEWRLPGCSMCLGM 413
QY 429 NPDLAPQERCASTSNRNEGROGAGRTHLMSPVMAAGIYVKLADVRKL 480
DB 414 NNDKLSGDERCASTSNRNFEGROGRGTRHLVSPIMAAAA-IYGHFVDVVRNL 464

RESULT 20
Q9EVF9 PRELIMINARY; PRT; 448 AA.
AC Q9EVF9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE Isopropylmalate dehydratase subunit (Fragment).
GN LEUC.
OS Buchnera aphidicola.
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
OX NCBI_TaxID=9;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=AP.
RX MEDLINE=20576185; PubMed=11133977;
RA Wernegreen J.J., Moran N.A.;
RT "Vertical transmission of biosynthetic plasmids in aphid endosymbionts (Buchnera).";
RL J. Bacteriol. 183:785-790 (2001).
DR EMBL; AF197457; AAG31406.1; -.
DR InterPro; IPR001030; Aconitase_N.
DR InterPro; IPR004430; LeuC.
DR Pfam; PF00330; aconitase; 1.

DR PRINTS; PR00415; ACONITASE.
DR ProDom; PD000511; Aconitase_N; 1.
DR TIGRfams; TIGR00170; leuC_1.
DR PROSITE; PS00415; ACONITASE_1; 1.
DR PROSITE; PS00450; ACONITASE_1; 1.
DR PROSITE; PS01244; ACONITASE_2; 1.
DR isomerase; Plasmid.
KW NON TER 448 448
SQ SEQUENCE 448 AA; 49936 MW; 0137DA4418C29779 CRC64;

Query Match 32.4%; Score 1315.5; DB 2; Length 448;
Best Local Similarity 57.1%; Pred. No. 1.3e-80;
Matches 260; Conservative 70; Mismatches 116; Indels 9; Gaps 4;

QY 9 QTLVDKVLQAHVDEKLDGTLLYIDRHLVHEVTSPOAFEGRLNAGRKVRPDCDTLATTD 68
DB 3 KTLVDKLYDSHVVEEKNISLTYIDLHLVHEVASPOAFDSLDRKNRKVRPDKTFTAMD 62
QY 69 HNVPTTSRKALKDIASFTEKEDDSTQCVTLLENVKEFGVTFGLSDRQGIHVHVGPEQG 128
DB 63 HNVSTTS---QDINA--SGSMAKVQMOELIKNCESEFNISLYDIKNPNQGIHVHVSPEKG 116
QY 129 FTLPGTTVCGDSTHTHGAFALFGIGTSEVHVLATQCLITKRSKNMRIQVDGELAP 188
DB 117 MTLPGMTIVCGDSTHTHGAFALSGFGIGTSEVHVLATQTLKQORFKNMKIEITGTQK 176
QY 189 GVSKDVLVHLAIGITAGGTGAVIEFCGVSIRSLSEARMSICNMSIEGGARAGVAPD 248
DB 177 FVTAKDILFTIGKLGSSGAGVIEFCGNVIEKMSNEERTICNMAIEGAKSGLIAPD 236
QY 249 EITEYLLKGRPLAPKYDSEPHKATQYWKQLQSDPGAKYDIDVIDAKDIVPTLTWTGSP 308
DB 237 EVTFYSYLLKNRYAPR--GVFWKKALNFWKNLKSDFKNAFFDKVWNINISDLSPOITWTGTP 294
QY 309 EDVVPITGVVPDPTFATEAKKADGRMLQYMGKAGTPEMEDI PVDKVFISGCTNSRIED 368
DB 295 DQVISIDQKIPDSSFDNLKDLAKSACKYMGKLTGTYLTNTITVDKVFISGCTNSRIED 354
QY 369 LRAAAAVVGRKKAPNVKSAWVPGSLVKTQAEELGDKIFEBAGFEWREAGSCMLGM 428
DB 355 LRAASKILDKKTIANNVK-AIIVPGSGSVKREANEGLDKIFINAGFEWRLPGCSMCLGM 413
QY 429 NPDLAPQERCASTSNRNEGROGAGRTHLMSPV 463
DB 414 NKDLNDGERCASHNRNFEGROGRXXRTHLVSP 448

RESULT 21
Q9PLW1 PRELIMINARY; PRT; 470 AA.
AC Q9PLW1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 3-isopropylmalate dehydratase large subunit (EC 4.2.1.33).
GN LEUC OR Cui1717C.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
OC Campylobacter.
OX NCBI_TaxID=197;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=NCYC 11168;
RX MEDLINE=20150912; PubMed=1068204;
RA Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,
RA Jagals K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
RA Whitehead S., Barrell B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT reveals hypervariable sequences.";
RL Nature 403:665-668 (2000).
DR EMBL; AL139079; CAB73703.1; -.
DR InterPro; IPR001030; Aconitase_N.
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DR EMBL; AL596171; CAC97326.1; -.
DR Listlist; LIN02096; -.
DR InterPro; IPR001030; Aconitase_N.
DR InterPro; IPR004430; Leuc.
DR Pfam; PF00330; aconitase; 1.
DR ProDom; PD000511; Aconitase_N; 1.
DR TIGRFAMs; TIGR00170; leuc; 1.
DR PROSITE; PS00450; ACONITASE_1; UNKNOWN_1.
DR PROSITE; PS01244; ACONITASE_2; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 462 AA; 51041 MW; 0F09F51E77F0B4B2 CRC64;

Query Match 31.7%; Score 1283.5; DB 16; Length 462;
Best Local Similarity 53.3%; Pred. No. 2e-78;
Matches 251; Conservative 72; Mismatches 129; Indels 19; Gaps

QY 9 QTLYDKVLQAHVDEKLDGTVLLYIDRHLVHEVTSPOAFEGRLNAGKVRPDCPTLATTD 68
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
3 KTLFDKLNHRVYKGEQEPQLLYIDLHLVHEVTSPOAFEGRLNAGKVRPDCPTLATMD 62
QY 69 HNVPTTSRKALKDIASFIKEDDSRTQCVTLLENVKEFGVTVFGLSKRQGIHVHVGPEQG 128
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
63 HNVPTEDIFNIQDLV-----AKQIEALQTNCEEFGLVTLADMGSDRQGIHVHVGPETG 115
QY 129 FTLPCTTVVCGDSHTSHGAFALAFGIGTSEVEHVLATQCLITKRSKNMRIQVDSGELAP 188
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
116 LTQPGKIVVCGDSHTATHGAFGAIFGIGTSEVEHVFATQTLWQTKPKMLKIDINGTLPT 175
QY 189 GVSSKDVVLHAIGTAGTGAIVFCGVSIRLSWEARMSICNMSIEGGARAGVAPD 248
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
176 GVYAKDIILHLIATYGVAFGTGVAVEYGTIRMSMEERTICNMAIEGGAKGGMWAPD 235
QY 249 EITFEYKGRPLAPKVDSPHMKATQYWKNSLOSPDCAKYDIDVDAKIDVPTLTWTGTS 308
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
236 QTFTEYVGRREYAPS----DMERAKRDWETLKTDPDAEYDLHIEMDASILEPVTWTG 291
QY 309 EDVVPITGVVPDETFATEAKKADGRMLQYMGKAGTPEMDIPVKVFTGSCNTRIED 368
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
292 EMGVPSKAFPP-----ETKDNMYERAYEYMGKPGQTAEIEELGVVFTGSCNTR 344
QY 369 LRAAAAIVKGRKKAPNVKSAMVVGSLVKTQAEIEGLDKIFEEAGFEWREACSCMCLGM 428
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
345 LEEAARIVKGNKYKNIR-ALVVGSRQVNAEAEALGLDKIFDAQFEWREPCSCMCLGM 403
QY 429 NPDIAPQERCASTSNRNFEGRQAGGRTHLMSFVMAAAGIVGKLADVRK 479
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
404 NPQVDPDGVHCASTSNRNFEGRQAGGRTHLVSPAMAAAAAINGHFDIRK 454

RESULT 24
Q99SJ3 PRELIMINARY; PRT; 456 AA.
AC Q99SJ3;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DE 3-isopropylmalate dehydratase large subunit.
GN LEUC OR SAV2059 OR SA1864.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Staphylococcus.
OX NCBI_taxid=158878, 158879;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
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RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
DR EMBL; AF003364; BAB58221.1; -.
DR EMBL; AP001336; BAB43146.1; -.
DR InterPro; IPR001030; Aconitase_N.
DR InterPro; IPR004430; Leuc.
DR Pfam; PF00330; aconitase; 1.
DR PRINTS; PR00415; ACONITASE.
DR ProDom; PD000511; Aconitase_N; 1.
DR TIGRFAMs; TIGR00170; leuc; 1.
DR PROSITE; PS00450; ACONITASE_1; 1.
DR PROSITE; PS01244; ACONITASE_2; 1.
KW Complete proteome.
SQ SEQUENCE 456 AA; 50326 MW; 4C2D584937186ECC CRC64;

Query Match 31.6%; Score 1282; DB 16; Length 456;
Best Local Similarity 54.4%; Pred. No. 2.5e-78;
Matches 257; Conservative 64; Mismatches 131; Indels 20; Gaps

QY 9 QTLYDKVLQAHVDEKLDGTVLLYIDRHLVHEVTSPOAFEGRLNAGKVRPDCPTLATTD 68
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
3 QTLFDKLNHRVYKGEQEPQLLYIDLHLVHEVTSPOAFEGRLNAGKVRPDCPTLATD 62
QY 69 HNVPTTSRKALKDIASFIKEDDSRTQCVTLLENVKEFGVTVFGLSKRQGIHVHVGPEQG 128
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
63 HNVPTI-----DIFN-IKDETANKOITLQKNAIDFGVHIFMGSDQGIHVHVGPETG 115
QY 129 FTLPCTTVVCGDSHTSHGAFALAFGIGTSEVEHVLATQCLITKRSKNMRIQVDSGELAP 188
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
116 LTQPGKTIIVCGDSHTATHGAFGAIFGIGTSEVEHVFATQTLWQTKPKMLKIDINGTLPT 175
QY 189 GVSSKDVVLHAIGTAGTGAIVFCGVSIRLSWEARMSICNMSIEGGARAGVAPD 248
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
176 GVYAKDIILHLIKTYGVDFGTGYALEFTGETTKNLSMDGRMTICNMAIEGGAKYGIQPD 235
QY 249 EITFEYKGRPLAPKVDSPHMKATQYWKNSLOSPDCAKYDIDVDAKIDVPTLTWTGTS 308
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
236 DITFEYVKGPRPADNF-----AKSVDKWRELYSDDDAIFDRVIELDVSTLEPQVTTG 290
QY 309 EDVVPITGVVPDETFATEAKKADGRMLQYMGKAGTPEMDIPVKVFTGSCNTRIED 368
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
291 EMGVNFSEPPF-----EINDINDQRAYDMGLEPGQAEIDILGYVFLGSCNTR 343
QY 369 LRAAAAIVKGRKKAPNVKSAMVVGSLVKTQAEIEGLDKIFEEAGFEWREACSCMCLGM 428
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
344 LLEASHIVKGNKVHPNI-TAIVVPGSRVTYKAEKLGDTIFKNAGFEWREPCSCMCLGM 402
QY 429 NPDIAPQERCASTSNRNFEGRQAGGRTHLMSFVMAAAGIVGKLADVRKL 480
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
403 NPQVDPDGVHCASTSNRNFEGRQAGGRTHLVSPAMAAAAAINGHFDVRKV 454

RESULT 25
Q99VH1 PRELIMINARY; PRT; 442 AA.
AC Q99VH1;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Isopropylmalate dehydratase subunit (Fragment).
GN LEUC.
OS Buchnera aphidicola.
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
OX NCBI_taxid=9;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UCAL;
RX MEDLINE=20576185; PubMed=11133977;
RA Wernegreen J.J., Moran N.A.;
RT "Vertical transmission of biosynthetic plasmids in aphid endosymbionts
```



Query Match	Best Local Similarity	Matches	Score	DB 2	Length	Gaps
Query 1	31.6%	56.0%	1280.5	DB 2	442	5
Query 2	31.6%	56.0%	1280.5	DB 2	442	5
Query 3	31.6%	56.0%	1280.5	DB 2	442	5
Query 4	31.6%	56.0%	1280.5	DB 2	442	5
Query 5	31.6%	56.0%	1280.5	DB 2	442	5
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Query 7	31.6%	56.0%	1280.5	DB 2	442	5
Query 8	31.6%	56.0%	1280.5	DB 2	442	5
Query 9	31.6%	56.0%	1280.5	DB 2	442	5
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Query 62						

Search completed: March 17, 2003, 08:50:17  
Job time : 50 secs

